

- 1 -

SEQUENCE LISTING

<110> THE UNIVERSITY OF QUEENSLAND

<120> A NOVEL PLANT PROMOTER AND USES THEREFOR

<130> 2209376/EJH

<140>

<141>

<150> PP5572

<151> 1998-08-31

<160> 9

<170> PatentIn Ver. 2.0

<210> 1

<211> 1923

<212> DNA

<213> Plant

<220>

<221> CDS

<222> (88)..(1539)

SEQ ID NO:1

atcctctctc ccacttactt cgatttcacg aattccaata aactcaacac actttttttac 60

actccacact ctaaccacat acaccat atg ggt ttc aag gcc atg gac caa act 114

Met Gly Phe Lys Ala Met Asp Gln Thr

1

5

ccc ttg ttg tcc aag atg gct att ggg gat gga cat ggc gaa tca tcc 162

Pro Leu Leu Ser Lys Met Ala Ile Gly Asp Gly His Gly Glu Ser Ser

10

15

20

25

cca tac ttt gat gga tgg aag gct tat gat caa aac ccc ttt cat ccc 210

Pro Tyr Phe Asp Gly Trp Lys Ala Tyr Asp Gln Asn Pro Phe His Pro

30

35

40

aca gat aat cct aac ggt gtt atg caa atg ggt ctt gct gag aat cag 258

Thr Asp Asn Pro Asn Gly Val Met Gln Met Gly Leu Ala Glu Asn Gln

45

50

55

ctt acc tct gat ttg gtt gaa gat tgg ata ctg aac aac cct gaa gcc 306

- 2 -

Leu Thr Ser Asp Leu Val Glu Asp Trp Ile Leu Asn Asn Pro Glu Ala	
60 65 70	
tcc att tgc act cca gaa gga ata aat gat ttc agg gcc ata gct aac	354
Ser Ile Cys Thr Pro Glu Gly Ile Asn Asp Phe Arg Ala Ile Ala Asn	
75 80 85	
ttt cag gat tat cat ggt ctg gcc gag ttc aga aat gct gtg gct aaa	402
Phe Gln Asp Tyr His Gly Leu Ala Glu Phe Arg Asn Ala Val Ala Lys	
90 95 100 105	
ttt atg gct aga aca agg gga aac aga atc acg ttt gac cct gac cgt	450
Phe Met Ala Arg Thr Arg Gly Asn Arg Ile Thr Phe Asp Pro Asp Arg	
110 115 120	
att gtc atg agc ggt gga gcc acc gga gca cac gaa gtc act gcc ttt	498
Ile Val Met Ser Gly Gly Ala Thr Gly Ala His Glu Val Thr Ala Phe	
125 130 135	
tgt ttg gca gat ccc ggc gag gca ttc tta gtg ccc att ccc tat tat	546
Cys Leu Ala Asp Pro Gly Glu Ala Phe Leu Val Pro Ile Pro Tyr Tyr	
140 145 150	
cca ggc ttt gac cgg gat ttg agg tgg aga aca gga gtt aaa ctt gtt	594
Pro Gly Phe Asp Arg Asp Leu Arg Trp Arg Thr Gly Val Lys Leu Val	
155 160 165	
cca gtt atg tgc gat agc tca aat aat ttc gtg ttg aca aag gaa gca	642
Pro Val Met Cys Asp Ser Ser Asn Asn Phe Val Leu Thr Lys Glu Ala	
170 175 180 185	
ttg gaa gat gcc tat gag aaa gca aga gag gat aac atc aga gta aag	690
Leu Glu Asp Ala Tyr Glu Lys Ala Arg Glu Asp Asn Ile Arg Val Lys	
190 195 200	
ggt tta ctg atc acc aat cca tca aat cca tta ggc aca atc atg gac	738
Gly Leu Leu Ile Thr Asn Pro Ser Asn Pro Leu Gly Thr Ile Met Asp	
205 210 215	
aga aag aca ctg aga acc gtg gtg agc ttc atc aat gag aag cgt atc	786
Arg Lys Thr Leu Arg Thr Val Val Ser Phe Ile Asn Glu Lys Arg Ile	
220 225 230	
cac ctt gta tgt gat gaa ata tat gct gca aca gtt ttc agc caa ccc	834
His Leu Val Cys Asp Glu Ile Tyr Ala Ala Thr Val Phe Ser Gln Pro	
235 240 245	

- 3 -

ggt ttc ata agc ata gct gag ata tta gag gat gaa aca gac ata gag	882
Gly Phe Ile Ser Ile Ala Glu Ile Leu Glu Asp Glu Thr Asp Ile Glu	
250 255 260 265	
tgt gac cgc aac ctc gta cac att gtt tat agt ctt tca aag gac atg	930
Cys Asp Arg Asn Leu Val His Ile Val Tyr Ser Leu Ser Lys Asp Met	
270 275 280	
ggg ttc cct ggc ttc aga gtc ggc atc ata tac tct tac aat gat gct	978
Gly Phe Pro Gly Phe Arg Val Gly Ile Ile Tyr Ser Tyr Asn Asp Ala	
285 290 295	
gtg gtt aat tgt gca cgc aaa atg tca agc ttt gga ttg gtg tca aca	1026
Val Val Asn Cys Ala Arg Lys Met Ser Ser Phe Gly Leu Val Ser Thr	
300 305 310	
cag act cag tat ctt tta gca tcg atg cta aat gat gat gag ttt gtg	1074
Gln Thr Gln Tyr Leu Leu Ala Ser Met Leu Asn Asp Asp Glu Phe Val	
315 320 325	
gag agg ttt ctg gca gag agt gca aag agg ttg gct caa agg ttc agg	1122
Glu Arg Phe Leu Ala Glu Ser Ala Lys Arg Leu Ala Gln Arg Phe Arg	
330 335 340 345	
gtt ttc act ggg ggg ttg gcc aaa gtt ggc ata aag tgc ttg caa agc	1170
Val Phe Thr Gly Gly Leu Ala Lys Val Gly Ile Lys Cys Leu Gln Ser	
350 355 360	
aat gct ggt cta ttt gtg tgg atg gat tta agg caa ctt ctc aaa aag	1218
Asn Ala Gly Leu Phe Val Trp Met Asp Leu Arg Gln Leu Leu Lys Lys	
365 370 375	
cca act ttc gac tct gaa acg gag ctt tgg aaa gtt atc att cat gaa	1266
Pro Thr Phe Asp Ser Glu Thr Glu Leu Trp Lys Val Ile Ile His Glu	
380 385 390	
gtt aag atc aat gtt tca cct ggc tat tcc ttc cat tgc act gag cca	1314
Val Lys Ile Asn Val Ser Pro Gly Tyr Ser Phe His Cys Thr Glu Pro	
395 400 405	
ggg tgg ttt agg gtg tgc tat gcc aac atg gat gat atg gct gtg caa	1362
Gly Trp Phe Arg Val Cys Tyr Ala Asn Met Asp Asp Met Ala Val Gln	
410 415 420 425	
att gct ttg caa cga atc cgc aac ttt gtg ctt caa aac aag gag gtc	1410
Ile Ala Leu Gln Arg Ile Arg Asn Phe Val Leu Gln Asn Lys Glu Val	

- 4 -

430	435	440	
gtg gtg tct aat aag aaa cat tgt tgg cac agt aac ttg agg ctg agc			1458
Val Val Ser Asn Lys Lys His Cys Trp His Ser Asn Leu Arg Leu Ser			
445	450	455	
ctc aaa acc aga agg ttt gat gat atc acc atg tca cct cac tct ccc			1506
Leu Lys Thr Arg Arg Phe Asp Asp Ile Thr Met Ser Pro His Ser Pro			
460	465	470	
cta cct cag tca cct atg gtt aaa gcc aca aat tgagtttgca tattcctctg			1559
Leu Pro Gln Ser Pro Met Val Lys Ala Thr Asn			
475	480		
aatcgtttag aagaagtaac tgatatgtga agattacttg gttcttttat ttgttatttt			1619
gagaaggtac ataagtgctg gatttgttct ttggaacagc aataacagga aattcctgat			1679
gttgttttgt gatcggcatc acaatccagt gtcctacaag ttgtgctgct tcatgcacgc			1739
cccttcaatc ttaggggcat tttttctttt ttcacttacc aaaggttcaa ggtgaaaaaa			1799
gtttatagag tctgtaatgt tattggttta tcagaagagt ccaaagatg tctgtaatct			1859
gctactgaaa ttgtaacttt caattatgaa taaattgtta ataaaggtct tcaaattcat			1919
ttcc			1923

<210> 2
 <211> 484
 <212> PRT
 <213> Plant

SEQ ID NO:2

Met Gly Phe Lys Ala Met Asp Gln Thr Pro Leu Leu Ser Lys Met Ala			
1	5	10	15
Ile Gly Asp Gly His Gly Glu Ser Ser Pro Tyr Phe Asp Gly Trp Lys			
20	25	30	
Ala Tyr Asp Gln Asn Pro Phe His Pro Thr Asp Asn Pro Asn Gly Val			
35	40	45	
Met Gln Met Gly Leu Ala Glu Asn Gln Leu Thr Ser Asp Leu Val Glu			
50	55	60	

- 5 -

Asp	Trp	Ile	Leu	Asn	Asn	Pro	Glu	Ala	Ser	Ile	Cys	Thr	Pro	Glu	Gly	65	70	75	80
Ile	Asn	Asp	Phe	Arg	Ala	Ile	Ala	Asn	Phe	Gln	Asp	Tyr	His	Gly	Leu	85	90	95	
Ala	Glu	Phe	Arg	Asn	Ala	Val	Ala	Lys	Phe	Met	Ala	Arg	Thr	Arg	Gly	100	105	110	
Asn	Arg	Ile	Thr	Phe	Asp	Pro	Asp	Arg	Ile	Val	Met	Ser	Gly	Gly	Ala	115	120	125	
Thr	Gly	Ala	His	Glu	Val	Thr	Ala	Phe	Cys	Leu	Ala	Asp	Pro	Gly	Glu	130	135	140	
Ala	Phe	Leu	Val	Pro	Ile	Pro	Tyr	Tyr	Pro	Gly	Phe	Asp	Arg	Asp	Leu	145	150	155	160
Arg	Trp	Arg	Thr	Gly	Val	Lys	Leu	Val	Pro	Val	Met	Cys	Asp	Ser	Ser	165	170	175	
Asn	Asn	Phe	Val	Leu	Thr	Lys	Glu	Ala	Leu	Glu	Asp	Ala	Tyr	Glu	Lys	180	185	190	
Ala	Arg	Glu	Asp	Asn	Ile	Arg	Val	Lys	Gly	Leu	Leu	Ile	Thr	Asn	Pro	195	200	205	
Ser	Asn	Pro	Leu	Gly	Thr	Ile	Met	Asp	Arg	Lys	Thr	Leu	Arg	Thr	Val	210	215	220	
Val	Ser	Phe	Ile	Asn	Glu	Lys	Arg	Ile	His	Leu	Val	Cys	Asp	Glu	Ile	225	230	235	240
Tyr	Ala	Ala	Thr	Val	Phe	Ser	Gln	Pro	Gly	Phe	Ile	Ser	Ile	Ala	Glu	245	250	255	
Ile	Leu	Glu	Asp	Glu	Thr	Asp	Ile	Glu	Cys	Asp	Arg	Asn	Leu	Val	His	260	265	270	
Ile	Val	Tyr	Ser	Leu	Ser	Lys	Asp	Met	Gly	Phe	Pro	Gly	Phe	Arg	Val	275	280	285	
Gly	Ile	Ile	Tyr	Ser	Tyr	Asn	Asp	Ala	Val	Val	Asn	Cys	Ala	Arg	Lys	290	295	300	
Met	Ser	Ser	Phe	Gly	Leu	Val	Ser	Thr	Gln	Thr	Gln	Tyr	Leu	Leu	Ala	305	310	315	320

- 6 -

Ser Met Leu Asn Asp Asp Glu Phe Val Glu Arg Phe Leu Ala Glu Ser
325 330 335

Ala Lys Arg Leu Ala Gln Arg Phe Arg Val Phe Thr Gly Gly Leu Ala
340 345 350

Lys Val Gly Ile Lys Cys Leu Gln Ser Asn Ala Gly Leu Phe Val Trp
355 360 365

Met Asp Leu Arg Gln Leu Leu Lys Lys Pro Thr Phe Asp Ser Glu Thr
370 375 380

Glu Leu Trp Lys Val Ile Ile His Glu Val Lys Ile Asn Val Ser Pro
385 390 395 400

Gly Tyr Ser Phe His Cys Thr Glu Pro Gly Trp Phe Arg Val Cys Tyr
405 410 415

Ala Asn Met Asp Asp Met Ala Val Gln Ile Ala Leu Gln Arg Ile Arg
420 425 430

Asn Phe Val Leu Gln Asn Lys Glu Val Val Val Ser Asn Lys Lys His
435 440 445

Cys Trp His Ser Asn Leu Arg Leu Ser Leu Lys Thr Arg Arg Phe Asp
450 455 460

Asp Ile Thr Met Ser Pro His Ser Pro Leu Pro Gln Ser Pro Met Val
465 470 475 480

Lys Ala Thr Asn

<210> 3

<211> 2474

<212> DNA

<213> Plant

SEQ ID NO:3

ttacagatac acagaatcag acgacacatc tactttaata acagaaaaat aataagtgtc 60

ggagattatg gtacgacaag atgaaatgtt tttatatggt tgagattatt ttggtctgtt 120

gttggaagtt tcacgaatca tgattttgat tttacgtatt aaaaaatgaa aagttgaatc 180

- 7 -

atgcatttta tctagaagct gggaactgaa ccaaaaaaat agccagttga acaactgcag 240
tatttgtagg cgtattcatt tctcctttcc tacaataatc cttggttgct ctttatcgga 300
aaaaaaccaa aagcaatagc tactctgtaa ggtcctcgat tgccgacaag aacatcacat 360
gcgtgctgtc gaagaacaca taattttgag gttgaagctc acgtgcgagt tttgcatatt 420
tttaggttat gtgtacacgt atggagtgag ttccgcgtat atagtgtagg tagttgagtg 480
gctgagtagc gagtgaatca ggtaacacta tcttttcaag ccacctaatt aagggattta 540
atgttcatgc aactgttctt cgctaactaa ggccccactt acctttataa tattctctct 600
aactccgggc ttttggttaag tacaactttt ctactcttat ttaatggagg gattatTTTT 660
tccatatacc aattaattta ttttttaatt tatgcatttt gatcttatat taaaacaatt 720
atggtatgga ttaagtcgta tatcggtgac aattgaagtt ttcctcaagt ttagccattt 780
ttatgaaatt aaacttaatc actactatta ggtaaattca tatgtatcat taacaatttc 840
aatgtgagtt caattttacc caagatttga aagttgttgt caacttctgt taactaaagt 900
tgtattataa ggttgacgac tttaacctaa atctatTTTg aattgaaggg gttgatgact 960
tcagctttaa aataattcaa cttaaagttct agactacatt ggagatttta gtgttcataa 1020
aattttagaa aaaggctgag ttaaagttat gaaaaagatt ggtgactatt caattaatta 1080
gttgatgaatt gatgacaaat atttcatgag cataaccaat cagagaaata ccacctcgac 1140
cgactacaac aatctcaatg ttaattaatg aagcattgta gtataaggag tctagaataa 1200
atttcttaaa tattagagga aaactatTTT taaaaaatta caagaaaagt ttgatctata 1260
acctctttaa acttttaaatt atctaacaat tttcttatga ctacattgt gttgataggg 1320
tgattttgtc aaaatatatg tctatTTTat actagtatga tttgtctgcg aattatatat 1380
agtattaact tggagaaatg attgcctaat aagttataaa aaaggagaaa atatttattc 1440
ataaaaaaaaa tacacttaaa taagtaacaa taataaaaaa cattatataa gagattaaga 1500
taatttaata agtattgaat gtagaataat ttttatTTat aaatttgaac taaaatattc 1560

- 8 -

aaataatatt caaagtaa ataatagatata attcatcatt caatacgagt aattcaatct 1620
attataatca tatattagat aaatatacaa atatttgtaa aattttacat tattatatta 1680
ctaaatatat attaatttct ttgaatatct tttatacaag taggtagact agaagaatta 1740
tcttatctcc cgtatatttg tagatgttaa atgtaacggg ctagactga tgtttttgta 1800
ttatattatt tataaatcca ttagagattt aagttaatgt ctctctttga ttttaacatg 1860
gttctaaaaa ttaggtttta tcattgcgtc ctcaatgaac ccatgctata tgtttttaaag 1920
ttttttgttt ttgacaatg ttttttattt ctgagattgc tcttaggatt gaaattatgt 1980
ttgatactag aaaacgaaga agtagagagt agtgtataca cgtgtaaaaa ataatagttg 2040
tggaactta agttggattt gaatactagg acgaggctgg aagggtttcc actaagttga 2100
caaaaattat tacaagtggc aactagctag gtctcacaaa gtattactaa ttaatagtgg 2160
gtctgtctgc ataccaactc ttgctaatt ttcaaacc gcattctctc ttcttctctc 2220
cttcttctc tggaacttc atcgatgtgg acttctgtct ctcaaaagtc aagctcaatt 2280
tatccaatgc attataaata cacactctcc ctcccttcta ttcttcattg catcacattt 2340
cctctataaa ttactcacac cttattccta acttcatttc aacatcctct ctcccactta 2400
cttcgatttc atcaattcca ataaactcaa cacacttttt tacactccac actctaacca 2460
catacaccat atgg 2474

<210> 4
<211> 29
<212> DNA
<213> Plant

SEQ ID NO:4
gcggatccat cttggacaac aaggaggtt

29

<210> 5
<211> 30
<212> DNA
<213> Plant

- 9 -

SEQ ID NO:5

taggatccag aaagacactg agaaccgtgg

30

<210> 6

<211> 29

<212> DNA

<213> Plant

SEQ ID NO:6

acggatccgg tgtatgtggt tagagtgtg

29

<210> 7

<211> 29

<212> DNA

<213> Plant

SEQ ID NO:7

caggatccag acatagagtg tgaccgcaa

29

<210> 8

<211> 59

<212> DNA

<213> Plant

SEQ ID NO:8

atcgatcata tgagctctag acccgggctg caggatccgg tgtatgtggt tagagtgtg 59

<210> 9

<211> 57

<212> DNA

<213> Plant

SEQ ID NO:9

ccgcggagat ctatcgatct cgagaattca agcttcagac atagagtgtg accgcaa 57